

## AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning at page 9, line 34, with the following rewritten paragraph:

In a still further aspect, the invention provides a polypeptide produced by (i) hybridizing a test DNA molecule under stringent conditions with (a) a DNA molecule encoding a PRO1800 polypeptide having the sequence of amino acid residues from about 1 or about 16 to about 278, inclusive of ~~Figure 2 (SEQ ID NO: 3)~~ Figure 2 (SEQ ID NO:2), or (b) the complement of the DNA molecule of (a), and if the test DNA molecule has at least about an 80% sequence identity, preferably at least about an 85% sequence identity, more preferably at least about a 90% sequence identity, most preferably at least about a 95% sequence identity to (a) or (b), (ii) culturing a host cell comprising the test DNA molecule under conditions suitable for expression of the polypeptide, and (iii) recovering the polypeptide from the cell culture.

Please replace the entire section entitled "BRIEF DESCRIPTION OF THE DRAWINGS" beginning on page 35, line 15, with the following rewritten section:

### BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO1800 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA35672-2508".

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figure 1.

Figure 3 shows a nucleotide sequence (SEQ ID NO:6) of a native sequence PRO539 cDNA, wherein SEQ ID NO:6 is a clone designated herein as "DNA47465-1561".

Figure 4 shows the amino acid sequence (SEQ ID NO:7) derived from the coding sequence of SEQ ID NO:6 shown in Figure 3.

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Figure 5 shows a nucleotide sequence (SEQ ID NO:8) of a native sequence PRO982 cDNA, wherein SEQ ID NO:8 is a clone designated herein as "DNA57700-1408".

Figure 6 shows the amino acid sequence (SEQ ID NO:9) derived from the coding sequence of SEQ ID NO:8 shown in Figure 5.

Figure 7 shows a nucleotide sequence (~~SEQ ID NO:12~~SEQ ID NO:10) of a native sequence PRO1434 cDNA, wherein ~~SEQ ID NO:12~~SEQ ID NO:10 is a clone designated herein as "DNA68818-2536".

Figure 8 shows the amino acid sequence (~~SEQ ID NO:13~~SEQ ID NO:11) derived from the coding sequence of ~~SEQ ID NO:12~~SEQ ID NO:10 shown in Figure 7.

Figure 9 shows a nucleotide sequence (~~SEQ ID NO:17~~SEQ ID NO:15) of a native sequence PRO1863 cDNA, wherein ~~SEQ ID NO:17~~SEQ ID NO:15 is a clone designated herein as "DNA59847-2510".

Figure 10 shows the amino acid sequence (~~SEQ ID NO:18~~SEQ ID NO:16) derived from the coding sequence of ~~SEQ ID NO:17~~SEQ ID NO:15 shown in Figure 9.

Figure 11 shows a nucleotide sequence (~~SEQ ID NO:19~~SEQ ID NO:17) of a native sequence PRO1917 cDNA, wherein ~~SEQ ID NO:19~~SEQ ID NO:17 is a clone designated herein as "DNA76400-2528".

Figure 12 shows the amino acid sequence (~~SEQ ID NO:20~~SEQ ID NO:18) derived from the coding sequence of ~~SEQ ID NO:19~~SEQ ID NO:17 shown in Figure 11.

Figure 13 shows a nucleotide sequence (~~SEQ ID NO:21~~SEQ ID NO:19) of a native sequence PRO1868 cDNA, wherein ~~SEQ ID NO:21~~SEQ ID NO:19 is a clone designated herein as "DNA77624-2515".

Figure 14 shows the amino acid sequence (~~SEQ ID NO:22~~SEQ ID NO:20) derived from the coding sequence of ~~SEQ ID NO:21~~SEQ ID NO:19 shown in Figure 13.

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Figure 15 shows a nucleotide sequence (~~SEQ ID NO:23~~SEQ ID NO:21) of a native sequence PRO3434 cDNA, wherein ~~SEQ ID NO:23~~SEQ ID NO:21 is a clone designated herein as "DNA77631-2537".

Figure 16 shows the amino acid sequence (~~SEQ ID NO:24~~SEQ ID NO:22) derived from the coding sequence of ~~SEQ ID NO:23~~SEQ ID NO:21 shown in Figure 15.

Figure 17 shows a nucleotide sequence (~~SEQ ID NO:25~~SEQ ID NO:23) of a native sequence PRO1927 cDNA, wherein ~~SEQ ID NO:25~~SEQ ID NO:23 is a clone designated herein as "DNA82307-2531".

Figure 18 shows the amino acid sequence (~~SEQ ID NO:26~~SEQ ID NO:24) derived from the coding sequence of ~~SEQ ID NO:25~~SEQ ID NO:23 shown in Figure 17.

Please replace the paragraph beginning at page 70, line 37, with the following rewritten paragraph:

Using the WU-BLAST2 sequence alignment computer program, it has been found that a portion of the full-length native sequence PRO1434 (shown in ~~Figure 10 and SEQ ID NO:13~~Figure 8 and SEQ ID NO:11) has certain amino acid sequence identity with the mouse nel protein precursor (NEL\_MOUSE). Accordingly, it is presently believed that PRO1434 disclosed in the present application is a newly identified nel homolog and may possess activity typical of the nel protein family.

Please replace the paragraph beginning at page 71, line 11, with the following rewritten paragraph:

Using WU-BLAST2 sequence alignment computer programs, it has been found that amino acids 41 to 487 of PRO1917 (shown in ~~Figure 14 and SEQ ID NO:20~~Figure 12 and SEQ ID NO:18) has certain amino acid sequence identity with an inositol phosphatase designated in the Dayhoff database as "AF012714\_1". Accordingly, it is presently believed that PRO1917 disclosed in

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the present application is a newly identified member of inositol phosphatase family and may possess enzymatic activity typical of inositol phosphatases.

Please replace the paragraph beginning at page 71, line 18, with the following rewritten paragraph:

Using the WU-BLAST2 sequence alignment computer program, it has been found that a portion of the full-length native sequence PRO1868 (shown in ~~Figure 16 and SEQ ID NO:28~~ Figure 14 and SEQ ID NO:20) has certain amino acid sequence identity with the human A33 antigen protein (P\_W14146). Accordingly, it is presently believed that PRO1868 disclosed in the present application is a newly identified A33 antigen homolog which may possess activity and/or expression patterns typical of the A33 antigen protein. The PRO1868 polypeptide may find use in the therapeutic treatment of inflammatory diseases as described above and colorectal cancer.

Please replace the paragraph beginning at page 71, line 32, with the following rewritten paragraph:

Using WU-BLAST2 sequence alignment computer programs, it has been found that a full-length native sequence PRO1927 (~~Figure 20; SEQ ID NO:26~~ Figure 18; SEQ ID NO:24) has certain amino acid sequence identity with the amino acid sequence of the protein designated "AB000628\_1" in the Dayhoff database. Accordingly, it is presently believed that PRO1927 disclosed in the present application is a newly identified member of the glycosyltransferase family of proteins and may possess glycosylation activity.